

[illegible]

**FIG. 7EE**





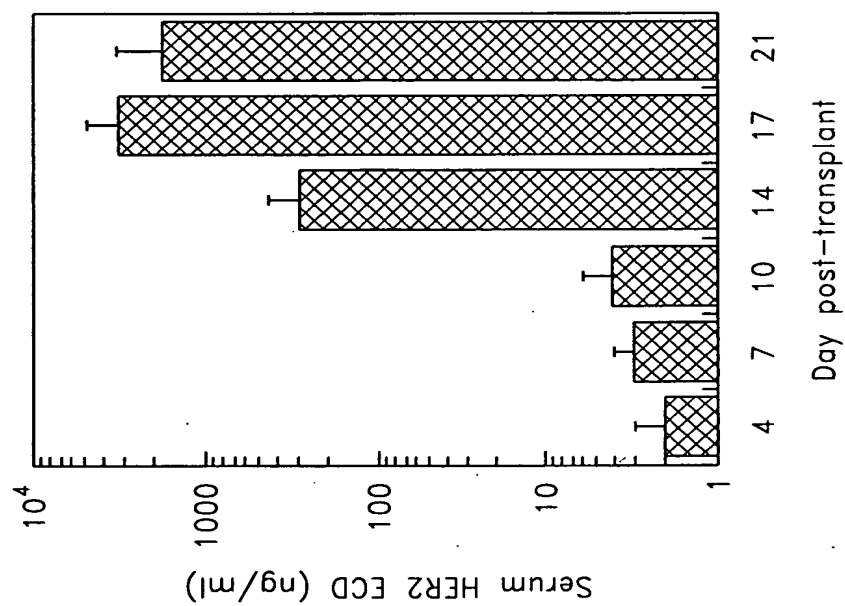


FIG. 8A

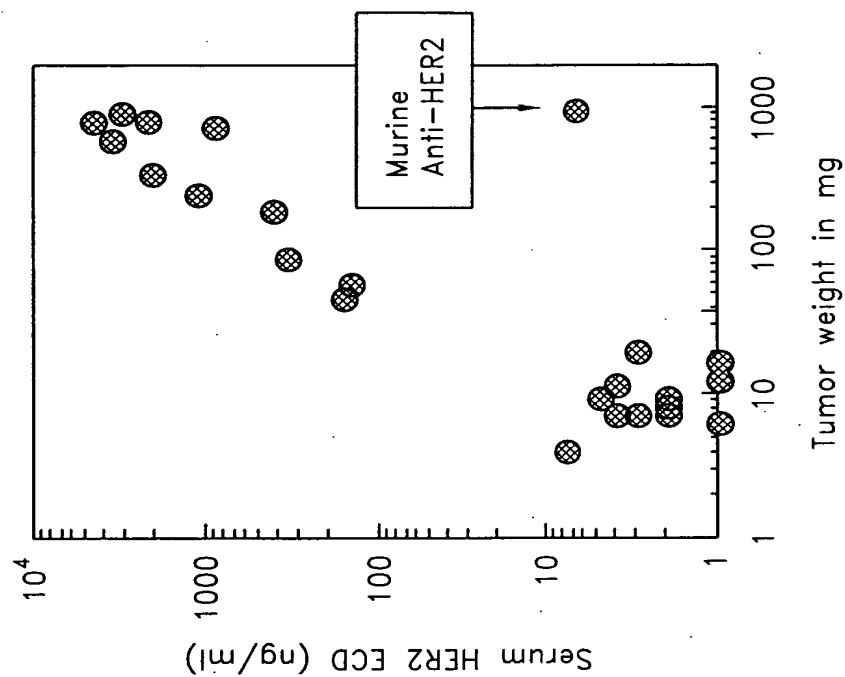


FIG. 8B

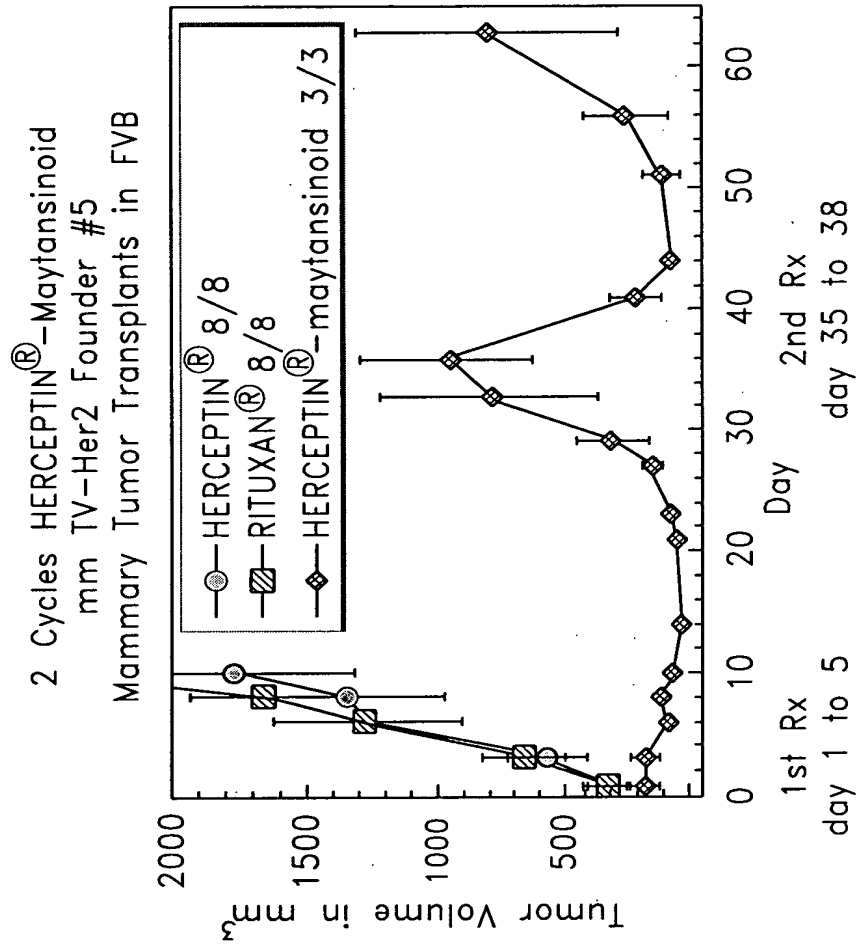


FIG. 9

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	Control IgG	FITC-Anti-HER2-V.P.	Both
HER2			
F05			
wnt <sup>1</sup>			
p53 <sup>+/+</sup>			

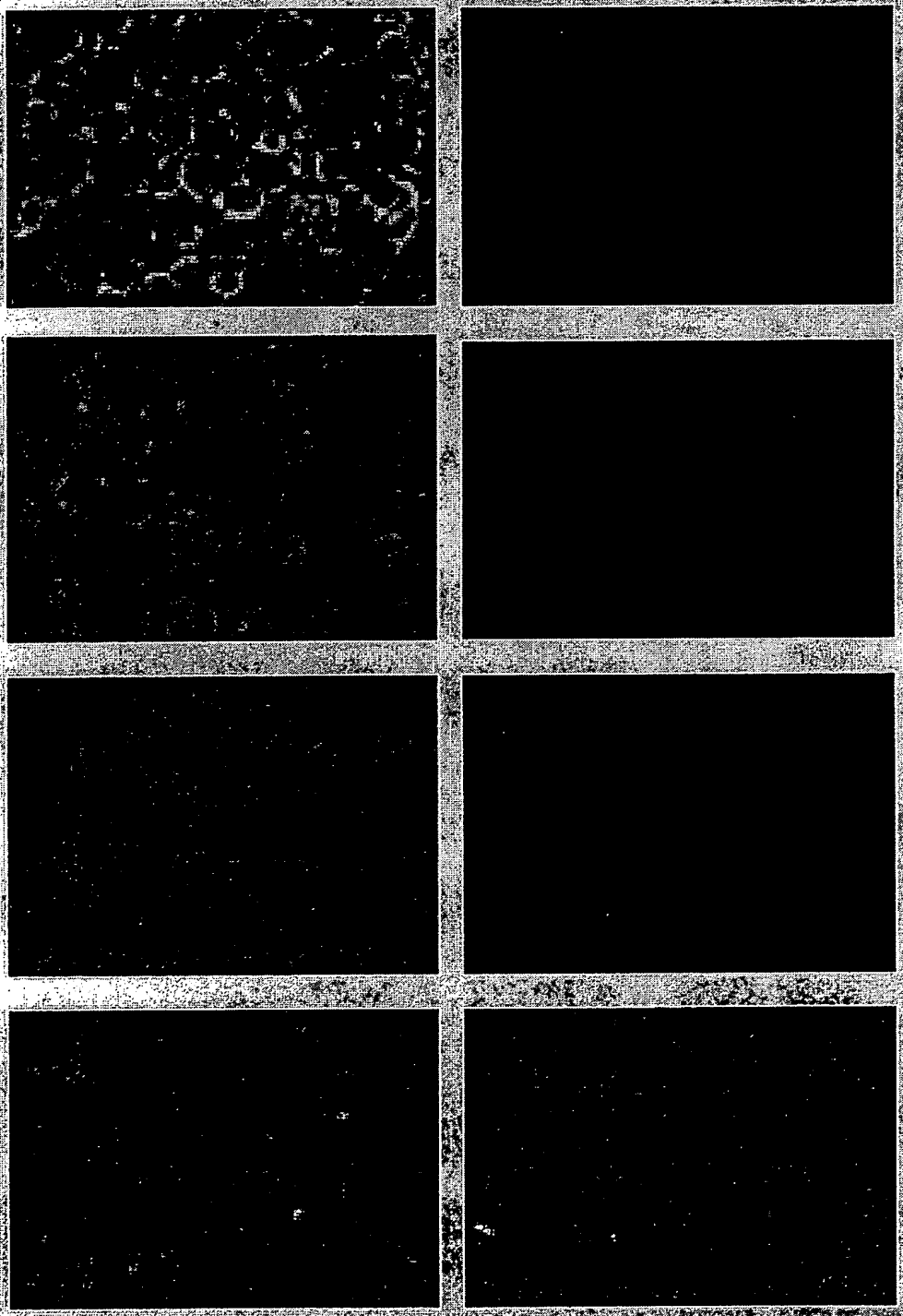


FIG. 10

FIG. 11

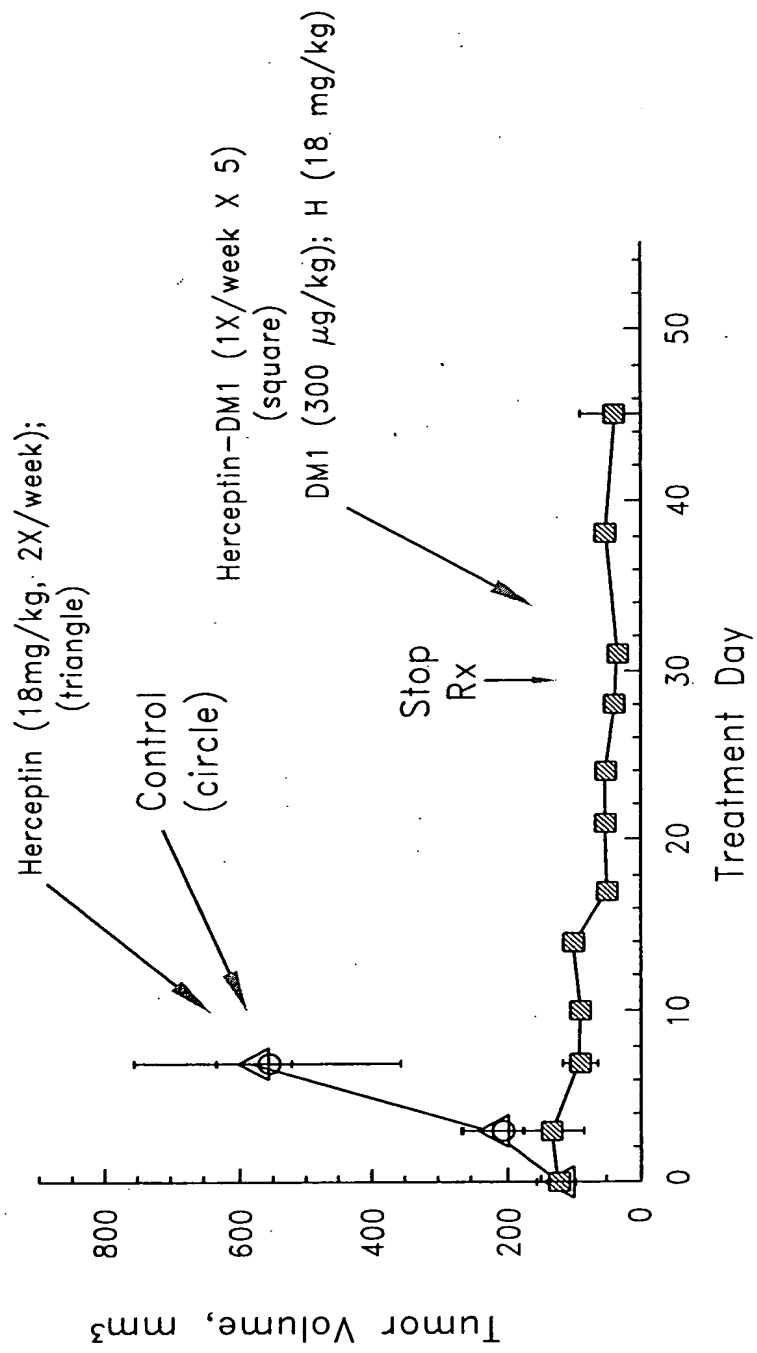


FIG. 11

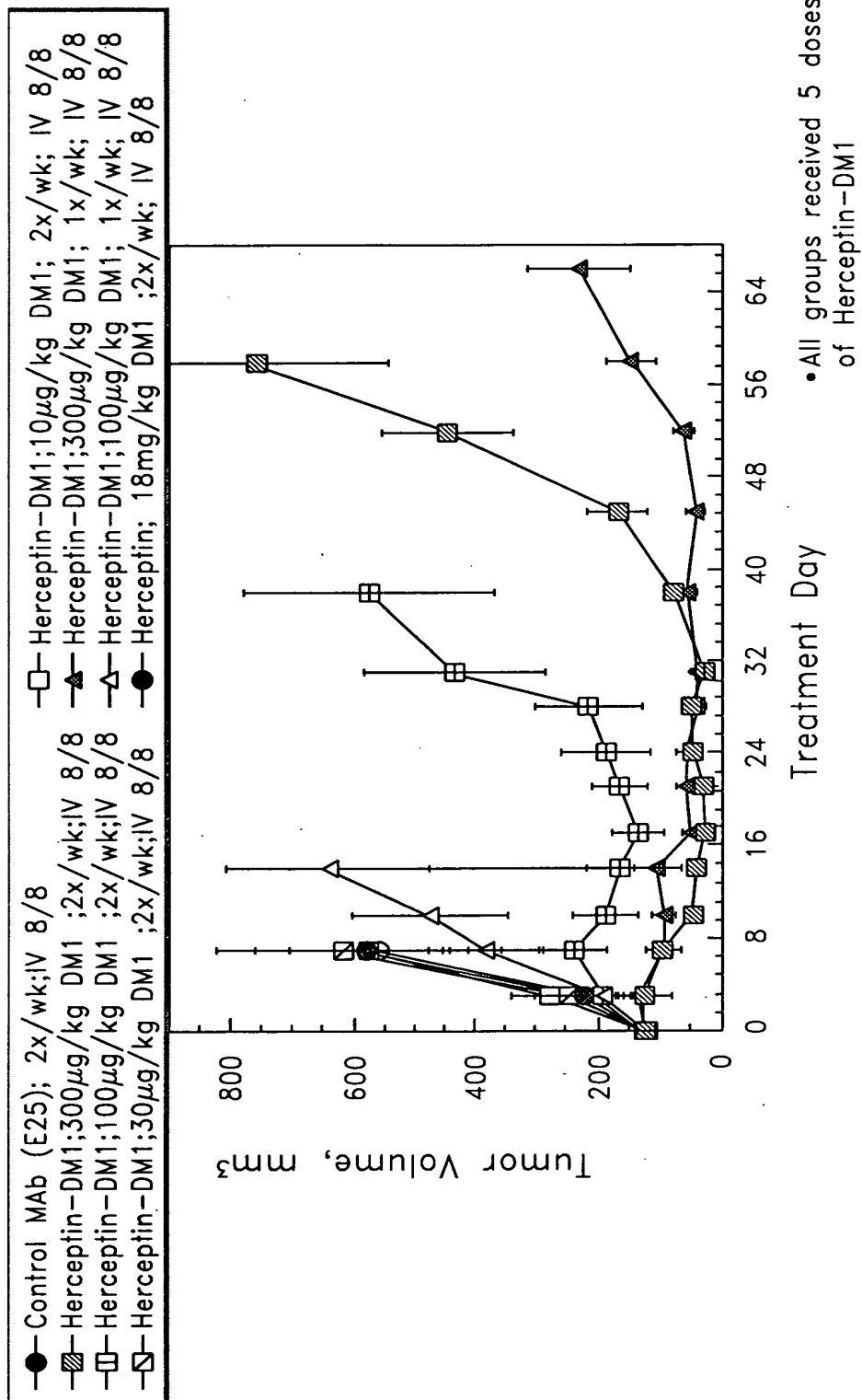


FIG. 12



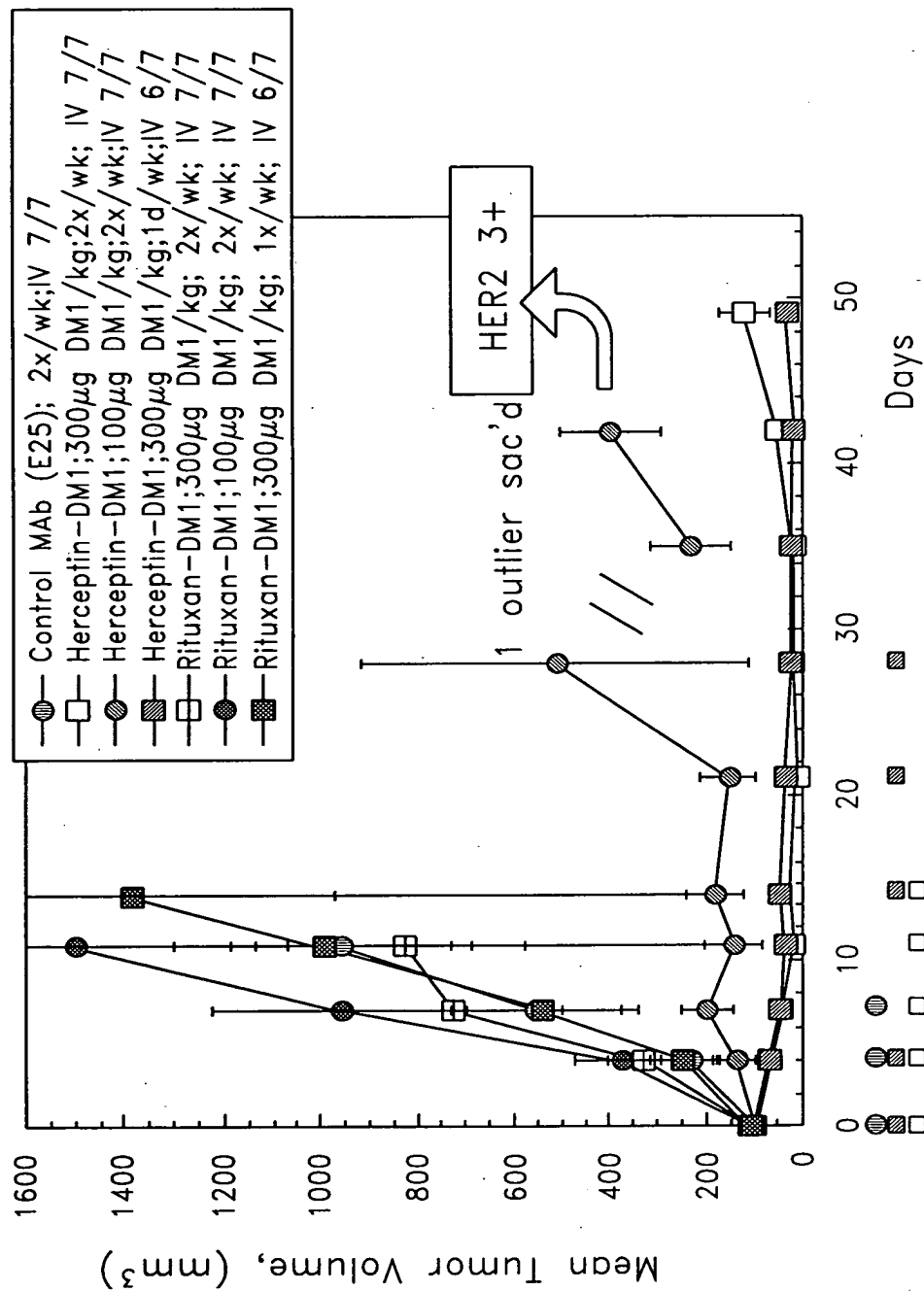


FIG. 13

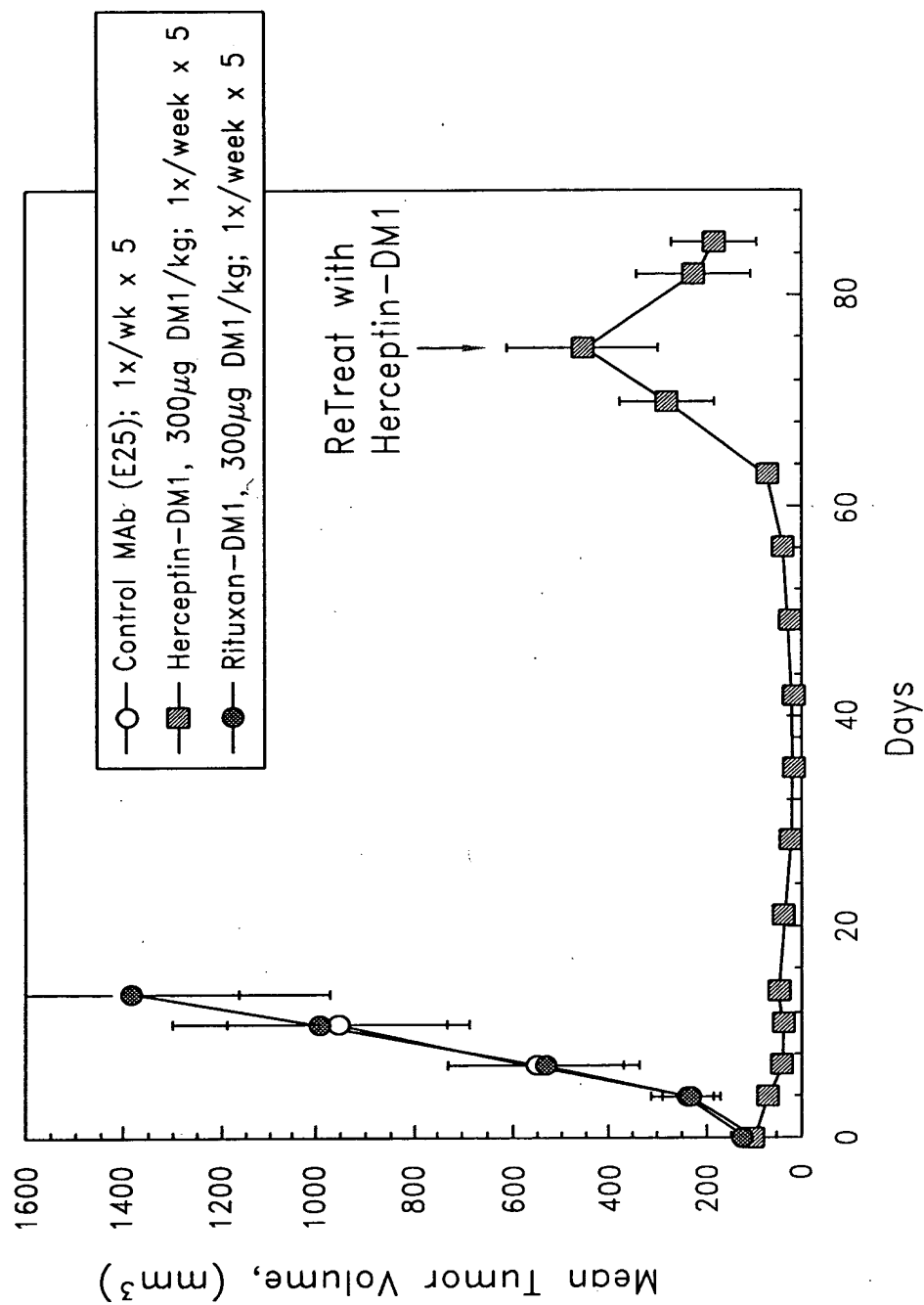


FIG. 14

5' -> 3' direction of the DNA sequence

rmaI  
 maeI  
 styI  
 bsaJI  
 blnI  
 avrII  
 haeIII/pal  
 stuI  
 haeI  
 mnII bfaI  
 mnII  
 mnII  
 bseRI  
 TTTGGAGGCC  
 TCTTCCGGT TCAGGCGTCT TCGGACTAC ACAGGAGTCC CTCGTCCCTT CCGCCGAGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAAA AACCTCCGG

sau96I  
 sau96I  
 pspOMI/bsp120I  
 nlaIV

hgiIII  
 thal haeIII/palI  
 fnuDII/mvnI  
 sacII/sstII  
 mspAII/nspBII  
 kspI bsp1286  
 dsaI bmyI  
 bsaJI asuI  
 fnu4HI/bsoFI  
 haeIII/palI  
 mcrI banII  
 eagI/smaII/eclXI  
 eaeI cac8I  
 cfrI acil

xhoI  
 smlI  
 pleI  
 taqI taqI  
 salI paeR7I

claiI/bsp106 hinfI rsaI maeI fnu4HI/bsoFI  
 aluI bspDI hincII/hindII csp6I bfaI acil bsh1236I  
 hindIII taqI accI avai scaI xbaI bsrBI acil apaI  
 TAGGCTTTTG CAAAAGCTT ATCGATACCG TCGACTCGAG AGTACTTCTA GAGCGGCCGC GGGCCCCATCG CCTCTGACAG CAACGTCTAT GACCTCCTAA  
 ATCCGAAAAC GTTTTTCGAA TAGCTATGGC AGCTGAGCTC TCATGAAGAT CTCGCCGCGC CCGGGGTAGC GGAGACTGTC GTTGACAGATA CTGGAGGATT  
 ^start of BS insert of HER2 xba-hindIII  
 ^end of human HER2 insert from BS at xhoI  
 ^start of hgh ex 4 (cla/nar)  
 ^TG PCR 5' pri

FIG. 7U

```

mspl
hpalI
scrFI
nciI
dsav
caulI
bssKI
bslI
tsei
fnu4HI/bsoFI
mnlI
mboII
bsrI
bglII
bstYI/xhoII
scfI
taqI

rmaI
maeI
bfalI
sau96I
avaII
asul
fokI
bstF5I
ppuMI
mnlI
sfaNI
eco0109I/draII
701 AGGACTAGAGGAAGGCATC CAAACGCTGA TGGGGAGGCT GGAAGATGGC AGCCCCCGGA CTGGGCAGAT CTTCAAGCAG ACCTACAGCA AGTTCGACAC
TCCTGGATCT CCTTCCGAG GTTTGCGACT ACCCCTCCGA CCTTCTACCG TCGGGGGCCT GACCCGCTA GAAGTTCGTC TGGATGTCGT TCAAGCTGTG
^end of ex 4/ start ex 5

801 AAACACAC AACGATGAC CACTACTCAA GAACTACGGG CTGCTCTACT GCTTCAGGAA GGACATGGAC AAGTCGAGA CATTCCTGCG CATCGTCGAC
TTTGATGTG TTGCTACTGC GTGATGAGTT CTTGATGCCC GACGAGATGA CGAAGTCTCTT CCTGTACCTG TTCCAGCTCT GTAAGGACGC GTAGCACGTC

```

[illegible][illegible]

**FIG. 7W**

[illegible][illegible]

**FIG. 7X**

```

scrFI
mvaI
ecorII
ecorII
dsav
bstNI
bssKI
apyI
    haeIII/palI
    mscI/balI
    haeI
    eaeI
        bsmAI
        bsal
        cfrI
            hphI
            cccCAAAGTG GTATAACCGG TCCGACCAGA GGTGAGGAT TAGAGTCCAC TAGATGGGTG GAACCGGAGG GTTAACGAC CCTAATGTCC GCACTTGGTG
            301 GGGGTTTCAC CATATTGGCC AGGCTGGTCT CCAACTCCTA ATCTCAGGTG ATCTACCCAC CTGGCCCTCC CAAATTGCTG GGATTACAGG CGTGAACCCAC
            tspRI
            mspI
            cfrI0I/bsrFI
            bsaWI
            styI
            sau96I hpaII
            ncoI haeIII/palI
            dsal asuI ageI
            bsaJI pflMI
            bspMI nlaIII bslI
            bsmFI
            401 TGCTCCCTTC CCTGTCCTTC TGATTTTAA ATAACCTATAC CAGCAGGAGG ACGTCCAGAC ACAGCATAGG CTACCTGCCA TGGCCCAACC GGTGGGACAT
            ACGAGGGAAG GGACAGGAAG ACTAAATTT TATTGATATG GTCGTCCTCC TGCAGTCTG TGTCGTATCC GATGGACGCT ACCGGGTGG CCACCCGTGA
            hgiAI/aspHI
            sau3AI
            mboI/ndeII
            tru9I
            dpnII bsp1286
            dpnI bsiHKAI
            tsp509I
            pvul/bspCI
            msei
            nlaIII
            mcrI
            bmyI
            aseI/asnI/vspI
            bsiEI
            apaII/snoI
            rcal
            apoI
            501 TTGAGTTGCT TGCTTGGCAC TGTCCTCTCA TGGGTTGGT CCACTCAGTA GATGCTGTGT GAATTACGAT CGGTGCACAT TAATTACATGA AATTCGTAAT
            AACTCAACGA ACGAACCGTG ACAGGAGAGT ACGCAACCCA GGTGAGTCAAT CATACCGACAA CTTAATGCTA GCCACGTGTA ATTAAGTACT TTAAGCATTA
            ^start of linker 2
            ^end of linker

```

**FIG. 7Y**





scrFI mwoI  
 mvaI thai  
 ecorII fnuDII/mvni  
 dsav bstUI  
 bstNI bsh1236I  
 bssKI aciI cac8I  
 nlaIII bsII apyI bsII  
 nsPHI cac8I apyI bsII  
 nsPI haeIII/palI HaeIII/palI fnu4HI/bsoFI  
 aflIII haeI haeI nlaIV haeIII/palI  
 901 CCGTAATACG GTTATCCACA GAATCAGGGG ATAACGGCAGG AAGCAACATG TGAGCAAAAG GCCAGCAAAA CGTAAAAAGG CCGCGTTGCT  
 GCCATTATCC CAATAGGTGT CTTAGTCCCC TATTGCGTCC TTTCTTGATC ACTCGTTTTC CCGTCGTTT CCGTCCTTTC GCATTTTCC GCGGCAACGA  
 scrFI  
 mvaI  
 ecorII  
 dsav  
 bstNI  
 bssKI  
 nlaIV  
 aciI  
 nlaIV  
 101 GCGTTTTTC CATAGGCTCC GCCCCTCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCCAGGCG  
 CCGCAAAAAG GTATCCGAGG CCGGGGACT GCTCGTAGTG TTTTGTAGCTG CGAGTTTCACT CTCCACCGCT TTGGGCTGTC CTGATATTTTCTC TATGTTCCGC  
 hgaI  
 drdI  
 taqI smlI mnlI  
 201 GCGTCTCAGC CTGTAGGTAT CTGAGTTTCGG TGTAGGTCTGT TCGTCTCAAG CTGGGCTGTG TGACGAAC CCCGTTTCAG CCCGCTTATC  
 TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTT GACCCGACAC AGTGCTTGG GGGGCAAGTC GGGCTGGCGA CCGGGAATAG  
 scrFI  
 mvaI  
 ecorII  
 dsav  
 bstNI  
 bssKI  
 apyI  
 bsaJI aluI mnlI hhaI/cfoI  
 101 TTTCCCCCTG GAAGTCCCT CGTGCGTCT CTGTTCCTGA CCTGCTCGCT TACCGGATAC CTGTCCGCT TTCTCCCTTC GGAAGCGTG GCGCTTTCTC  
 AAGGGGGAC CTTCCAGGGA GCACGGCGA GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGGCGA AAGAGGGAAG CCCTTCGCAC CCGGAAAGAG  
 hgiAI/aspHI  
 bsp1286  
 bsiHKAI  
 bmyI  
 hgiAI/aspHI  
 bsp1286  
 bsiHKAI  
 bmyI  
 tseI  
 fnu4HI/bsoFI  
 mspAI/nsbBII mspI  
 aciI hinPI hpaII  
 mcrI bbvI bsaWI  
 bsiEI hhaI/cfoI  
 201 AATGCTCAGC CTGTAGGTAT CTGAGTTTCGG TGTAGGTCTGT TCGTCTCAAG CTGGGCTGTG TGACGAAC CCCGTTTCAG CCCGCTTATC  
 TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTT GACCCGACAC AGTGCTTGG GGGGCAAGTC GGGCTGGCGA CCGGGAATAG  
 scfI ddeI  
 201 AATGCTCAGC CTGTAGGTAT CTGAGTTTCGG TGTAGGTCTGT TCGTCTCAAG CTGGGCTGTG TGACGAAC CCCGTTTCAG CCCGCTTATC  
 TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTT GACCCGACAC AGTGCTTGG GGGGCAAGTC GGGCTGGCGA CCGGGAATAG

FIG. 7AA

[illegible]

**FIG. 7BB**

701 CTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG  
 GAAAATTTAA TTTTACTTC AAAATTAGT TAGATTTTCAT ATATACTCAT TTGAACCAGA CTGTCAATGG TTACGAATTA GTCACTCCGT GGATAGAGTC

701 CTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG  
 GAAAATTTAA TTTTACTTC AAAATTAGT TAGATTTTCAT ATATACTCAT TTGAACCAGA CTGTCAATGG TTACGAATTA GTCACTCCGT GGATAGAGTC

801 CGATCTGTCT ATTTCTGTCA TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACTACGA TACGGAGGG CTTACCATCT GCCCCAGTG CTGCAATGAT  
 GCTAGACAGA TAAAGCAAGT AGGTATCAAC GGAAGTGGG GCAGCACATC TATTGATGCT ATGCCCTCCC GAATGGTAGA CCGGGGTAC GACGTACTA

901 ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG GCCCGAGGCG AGAAGTGGTC CTGCAACTTT ATCCGCCCTCC  
 TGGCGCTCTG GGTGGAGTG GCCGAGTCT AAATAGTCTT TATTGGTCTC CGGGCTCGG TCTTACCAG GACGTTGAAA TAGGCGGAGG

001 ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCCGCAAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC TGCTGGCATC GTGGTGTAC  
 TAGGTACAGT AATTAACAAC GGCCCTTCGA TCTCATTCTA CAAGCGGTCA ATTATCAAC GGTGTGCAAC AACGTTAAG ACAGCGTAG CACCACAGT

FIG. 7CC

FIG. 7DD

"The first step was to identify the regions of the genome that were most likely to be involved in the process of gene expression. This was done by comparing the expression levels of genes in different tissues and cell types. The results showed that certain regions of the genome were highly expressed in specific tissues, suggesting that these regions may be involved in the regulation of gene expression."

```

sau96I
avaII
asuI
nlaIV
scrFI
draIII mvaI
mwoI bsp1286 bsmFI
bstAPI bmyI ecorII
hgiAI/aspHI dsav
bsp1286 nlaIV bstNI
bsiHKAI hgiCI bssKI
bmyI banI bsaJI
apaLI/snoI apyI
alw44I/snoI bsaJI aluI nlaIV acilI
mnII
sau96I foki
haeIII/palI
asuI bstF5I
mnII bsrI tspRI bsrI mnII
ddeI bsrI tspRI bsrI mnII
101 ACTGAGGGAA CTGGCAGTG GACTGGCCT CATCCACCAT AACACCCACC TCTGCTCGT GCACACGGTG CCCTGGGACC AGCTCTTTTCG GAACCCGCAC
TGACTCCCTT GACCCGTCAC CTGACCGGGA GTAGGTGGTA TTGTGGGTGG AGACGAAGCA CGTGTGCCAC GGGACCCCTGG TCGAGAAAGC CTTGGGCGTG
458 L R E L G S G L A L I H H N T H L C F V H T V P W D Q L F R N P H

haeIII/palI
scrFI
mvaI
ecorII
dsav
bstNI
bssKI
apyI
haeIII/palI
sau96I
asuI haeI
eco0109I/draII
mnII mwoI cac8I mspALI/bspBII mnII tspRI nlaIV eco0109I
201 CAAGCTCTGC TCCACACTGC CAACCGGCCA GAGGACGAGT GTCTGGGGCGA GGGCCTGGCC TGCCACCAGC TGTCGCCCGC AGGGCACTGC TGGGTCCAG
GTTTCGAGAG AGGTGTGACG GTTGGCGCGT CTCCTGTCTCA CACACCCGCT CCCGGACCGG ACGGTGGTGC ACACGGGGC TCCGTGACG ACCCCAGGTC
491 Q A L L H T A N R P E D E C V G E G L A C H Q L C A R G H C W G P G
sequence change from Coussens to Yamamoto^

sau96I
pspOMI
nlaIV
hgiJII
bsp1286
bmyI
banII
scrFI
mvaI
ecorII
dsav
bstNI
bssKI
bsaJI
apyI
sau96I
avaII asuI
asuI apaI
bcgI
bsaJI
avaI bsp1286
hinPI bmyI
aluI hhaI/cfoI
pvuII
mnII mspALI/bspBII mnII tspRI nlaIV eco0109I
201 CAAGCTCTGC TCCACACTGC CAACCGGCCA GAGGACGAGT GTCTGGGGCGA GGGCCTGGCC TGCCACCAGC TGTCGCCCGC AGGGCACTGC TGGGTCCAG
GTTTCGAGAG AGGTGTGACG GTTGGCGCGT CTCCTGTCTCA CACACCCGCT CCCGGACCGG ACGGTGGTGC ACACGGGGC TCCGTGACG ACCCCAGGTC
491 Q A L L H T A N R P E D E C V G E G L A C H Q L C A R G H C W G P G
sequence change from Coussens to Yamamoto^

```

FIG. 7K

[illegible]

**FIG. 7L**

3601 AGCCTTGCCC CATCACTGC ACCCACTCCT GTGTGGACCT GGATGACAAG GGCTGCCCGG CCGAGCAGAG AGCCAGCCCT CTGACGTCCA TCCTCTCTGC  
 TCGGAACGGG GTAGTTGACG TGGGTGAGGA CACACCTGGA CCTACTGTTC CCGACGGGGC GGCTCGTCTC TCGTGGGA GACTGCAGGT AGCAGAGACG  
 625 P C P I N C T H S C V D L D D K G C P A E Q R A S P L T S I V S A

scrFI  
 mvaI  
 ecorII  
 dsav  
 bstNI  
 bssKI  
 apyI  
 sau96I  
 avaiI foki  
 asuI bstF5I  
 mslI  
 tseI  
 fnu4HI/bsoFI  
 bbvI aciI  
 cac8I mnlI aatII bsmBI aciI  
 tail  
 maeII esp3I  
 hinII/acyI bsmAI  
 ahaiI/bsaHI

mspI  
 mroI  
 bspMII  
 bspEI  
 bsaWI  
 sau3AI  
 mboI/ndeII  
 dpnII  
 dpnI  
 alwI  
 bstYI/xhoII  
 tseI  
 fnu4HI/bsoFI hpaII rsaI  
 mwoI  
 bbvI mboII accIII csp6I sfaNI bsmAI bbvI  
 bsmI  
 GGTGGTTGGC ATTCTGCTGG TCGTGGTCTT GGGGTGGTC TTTGGGATCC TCATCAAGCG ACGGACGAG AGATACCGGA AGTACACGAT GCGGAGACTG  
 CCACCAACCG TAAGACGACC AGCACCAGAA CCCCACCAAG AAACCTAGG AGTAGTTGCG TGCCGTGCTC TTCTAGGCTC TCATGTGCTA CGCCTCTGAC  
 658 V V G I L L V V V L G V V F G I L I K R R Q Q K I R K Y T M R R L

FIG. 7M

FIG. 7N



[illegible]

**FIG. 70**



4601 ATGTTGGATG ATTGACTCTG AATGTCGGCC AAGATTCCGG GAGTTGGTGT CTGAATTCTC CCGCATGGCC AGGACCCCGG AGCGCTTTGT GGTCATCCAG  
TACAACCTAC TAACTGAGAC TTACAGCCGG TTCTAAGGCC CTCACCCACA GACTTAAGAG GGCTACCGG TCCCTGGGGG TCGCGAAACA CCAGTAGGTC  
958 C W M I D S E C R P R F R E L V S E F S R M A R D P Q R F V V I Q

4601 ATGTTGGATG ATTGACTCTG AATGTCGGCC AAGATTCCGG GAGTTGGTGT CTGAATTCTC CCGCATGGCC AGGACCCCGG AGCGCTTTGT GGTCATCCAG  
TACAACCTAC TAACTGAGAC TTACAGCCGG TTCTAAGGCC CTCACCCACA GACTTAAGAG GGCTACCGG TCCCTGGGGG TCGCGAAACA CCAGTAGGTC  
958 C W M I D S E C R P R F R E L V S E F S R M A R D P Q R F V V I Q

4701 AATGAGGACT TGGGCCACAG CAGTCCCTTG GACAGCACCT TCTACCGCTC ACTGCTGGAG GACGATGACA TGGGGGACCT GGTGGATGCT GAGGAGTATC  
TAACTCCTGA ACCCGGTCG GTCAGGGAAC CTGTCGTGGA AGATGGCGAG TGACGACCTC CTGCTACTGT ACCCCCTGGA CCACCTACGA CTCCTCATAG  
991 N E D L G P A S P L D S T F Y R S L L E D D M G D L V D A E E Y L

FIG. 7Q

[illegible]

FIG. 7B





sau3AI hgiAI/aspHI sau3AI maeI rmaI  
 mboI/ndeII tru9I dpnII nheI mboI/ndeII  
 dpnII bsp1286 dpnI cac8I tseI sphI fnu4HI/bsolFI  
 pvuI/bspCI mseI nlaIII thalI cac8I nspHI bbvI  
 mcrI bsiHKAI tsp509I fnuDII/mvnI cac8I scfI  
 bsiEI bmyI aseI/asnI/vspI bstUI bfaI aluI nspI pstI  
 taqI apaLI/snoI rcaI bsh1236I fnu4HI/bsolFI cac8I  
 aluI dpnI alw44I/snoI bspHI nruI aluI bbvI cac8I bsgI  
 1 AAGCTCGATC GGTGCACATT AATTCAATGAT CGCGAGCTAG CAGCTGTCAT GCCTGCAGCA GAAATGGTTG AACTCCCGAG AGTGTCTTAC ACCTAGGGGA  
 TTCGAGCTAG CCACGCTGTA TTAAGTACTA GCGCTCGATC GTCGAACGTA CGGACGTCGT CTTTACCAAC TTGAGGGCTC TCACAGGATG TGGATCCCTC  
 ~start of linker 1 ~end of linker 1 ~start of MMTV promoter

styI hgiJII  
 bsaJI bsp1286  
 tseI hinPI  
 fnu4HI/bsolFI hhaI/cfoI  
 bbvI mstI bmyI  
 styI bciGI avilI/fspI foki tseI  
 bsaJI ahdI/eam1105I bstF5I fnu4HI/bsolFI  
 101 GAAGCAGCCA AGGGGTGTT TCCACCAAG GACGACCCGT CTGGCGACAA ACGGTAGGC CCATCAGACA AAGACATATT CATTTCTCTGC TGCAAACTTG  
 CTTCTCGGT TCCCCAACAA AGGTGGTTC CTGCTGGGCA GACGCGTGT TGCCTACTCG GGTAAGTCTGT TCTGTATAA GTAAGAGACG ACGTTTGAAC

aluI mwoI  
 mwoI hgiJII  
 cac8I hgiAI/aspHI  
 bsp1286 bsp1286  
 bsiHKAI bmyI  
 bmyI banII hphI  
 mwoI acilI  
 mwoI bmyI  
 pleI tru9I sapI  
 maml earI/ksp632I  
 bsaBI msel aluI  
 201 GCATAGCTCT GCTTTGCTGG GGCATTGGG GAAAGTTGGG TTCGTGCTCG CAGGGCTCTC ACCCTTGACT CTTTAAATAG CTCTTCTGTG CAAGATTACA  
 CGTATCAGA CGAAACGACC CCGTAACCCC CTTCAACCCC AAGCACCAGC GTCCCGAGAG TGGGAACTGA GAAAATTATC GAGAAGACAC GTTCTAATGT

**FIG. 7A**

[illegible]

FIG. 7B



rmaI                   styI                   nlaIII                   rmaI  
 maeI                   bsaJI                   rsal                   maeI  
 bfaI                   mnlI                   csp6I                   bfaI                   bsmI  
 aluI                   mboII                   nlaIII  
 pleI                   smII                   nlaIII  
 hinfI                   bsmAI                   csp6I  
 801 AAAGACTCGC CAGAGCTAGA CCTCCTTGGT GTATGTTGTC TCAAGAAGAA AAAGACGACA TGAACAACA GGTACATGAT TATATTTATC TAGGAACAGG  
 TTTCTGAGCG GTCTCGATCT GGAGGAACCA CATAACAACAG AGTTCTTCTT TTTCTGCTGT ACTTTGTTGT CCATGTACTA ATATAAATAG ATCCTTGTC

tspRI  
 styI                   alwNI  
 bsII                   bsmFI  
 bsII bsaJI mnlI alw26I/bsmAI                   nlaIII  
 901 AATGCACTTT TGGGGAAGA TTTTCCATAC CAAGGAGGG ACAGTGGCTG GACTAATAGA ACATTATTCT GCAAAAACTT ATGGCATGAG TTATTATGAA  
 TTACGTGAAA ACCCCTTTCT AAAAGGTATG GTTCTCTCCC TGTCACCGAC CTGATTATCT TGTAATAAGA CGTTTTTGAA TACCGTACTC AATAATACTT

tru9I                   mseI                   fokI  
 sau96I                   styI                   bstF5I  
 haeIII/palI nlaIV                   tru9I                   mnlI                   bsmAI  
 asuI                   aciI                   bsaJI aflII/bfrI                   maeIII                   mnlI                   bsmAI  
 001 TAGCCTTTAT TGGCCCAACC TTGGGGTTCC CAAGGCTTAA GTAAGTTTTT GGTTACAAC TGTCTCTTAA ACAGAGGATGT GAGACAAGTG CTTTGGTGAC  
 ATCGGAAATA ACCGGGTTGG AACGCCAAGG GTTCCGAATT CATTCAAAA CCAATGTTG ACAAGAATTT TGTCTCTTACA CTCTGTTTAC CAAAGGACTG

sstI  
 sacI  
 hgiJII  
 hgiAI/aspHI  
 ecl136II  
 bsp1286  
 bsiHKAI  
 bmyI  
 ddeI  
 sau3AI  
 mboI/ndeII  
 dpnII aluI  
 dpnI banII ddeI  
 101 TTGGTTTGGT ATCAAAGGTT CTGATCTGAG CTCTGAGTGT TCTATTTTCC TATGTTCTTT TGGAAATTTAT CCAAAATCTTA TGTAATGCT TATGTAAACC  
 AACCAACCA TAGTTTCCAA GACTAGACTC GAGACTCACA AGATAAAGG ATACAAGAA ACCTTAAATA GGTTAGAAT ACATTTACGA ATACATTG

FIG. 7C

bsmAI  
 esp3I  
 foki bsmBI bsrBI tsp45I  
 bstF5I aciI maeIII  
 mnII  
 hphI  
 201 AAGATATAAA AGAGTGCTGA TTTTGTGAGT AAACCTTGCAA CAGTCCTAAC ATTCACCTCT TGTGTGTTTG TGTCTGTTCG CCATCCCGTC TCCGCTCGTC  
 TTCTATATTT TCTCAGCACT AAAAAACTCA TTGAACGTT GTCAGGATTG TAAAGTGAGA ACACACAAAC ACAGACAAGC GGTAGGGCAG AGGCGAGCAG  
 sau3AI  
 alwI  
 sau96I  
 nlaIV  
 avaiI  
 asuI  
 sanDI  
 ppuMI  
 nlaIV  
 ecoO109I/draII  
 mnII bsmFI aciI  
 bsaJI dpnI bfaI nruI bspDI hindIII bsiEI mseI bsgI  
 301 ACTTATCCTT CACTTTCCAG AGGGTCCCC CGCAGACCCC GGATCGCTAG CTCGCGAATC GATAGCTTG CGGCCGCTTA ACTGCAGAAG TTGGTCGTGA  
 TGAATAGGAA GTGAAGGTC TCCCAGGGGG GCGTCTGGGG CCTAGCGATC GAGCGCTTAG CTATTGCAAC GCCGGCGAAT TGACGTCTTC AACCAGCACT  
 ^start of BS intron insert at Cla  
 ^bp820 in pCI  
 ^start of BS insert at HindIII  
 pleI  
 hinFI  
 mboII  
 bsmAI  
 bpuAI  
 bbsI  
 taqI  
 bsrI  
 tru9I bsmAI  
 mseI bsaI  
 maeII  
 401 GGCACTGGGC AGGTAAGTAT CAAGGTATACA AGACAGGTTT AAGGAGACCA ATAGAACTG GGCTTGTCGA GACAGAGAAG ACTCTTGCCT TTCTGATAGG  
 CCGTGACCCG TCCATTGATA GTTCCAAATGT TCTGTCCAAA TTCCTCTGGT TATCTTTGAC CCGAACAGCT CTGTCTCTTC TGAGAACGCA AAGACTATCC  
 ^start of chimeric intron at pCI 857

**FIG. 7D**

501 CACCTATTGG TCTTACTGAC ATCCACTTTG CCTTCTCTCTC CACAGGTGC CACTCCCAGG TTCAATTACA GCTCTTAAGC GGCGCAAGC TTGATATCGA  
GTGGATAACC AGAATGACTG TAGGTGAAAC GGAAGAGAG GTGTCCACAG GTGAGGTGCC AAGTTAATGT CGAGAATTTCG CCGCGGTTTCG AACTATAGCT

501 CACCTATTGG TCTTACTGAC ATCCACTTTG CCTTCTCTCTC CACAGGTGC CACTCCCAGG TTCAATTACA GCTCTTAAGC GGCGCAAGC TTGATATCGA  
GTGGATAACC AGAATGACTG TAGGTGAAAC GGAAGAGAG GTGTCCACAG GTGAGGTGCC AAGTTAATGT CGAGAATTTCG CCGCGGTTTCG AACTATAGCT

^end of chimeric intron at pCI 989

end of BS insert at HindIII^

501 CACCTATTGG TCTTACTGAC ATCCACTTTG CCTTCTCTCTC CACAGGTGC CACTCCCAGG TTCAATTACA GCTCTTAAGC GGCGCAAGC TTGATATCGA  
GTGGATAACC AGAATGACTG TAGGTGAAAC GGAAGAGAG GTGTCCACAG GTGAGGTGCC AAGTTAATGT CGAGAATTTCG CCGCGGTTTCG AACTATAGCT

^end of chimeric intron at pCI 989

end of BS insert at HindIII^





191 A C H P C S P M C K G S R C W G E S S E D C Q S L T R T V C A G G C  
 201 GCCTGCCACC CCTGTCTCTCC GATGTGTAAG GGCTCCCGCT GCTGGGGGAGA GAGTTCTGAG GATTGTGAGA GCCTGACGCG CACTGTCTGT GCCGGTGGCT  
 211 CGGACGGTGG GGACAAGAGG CTACACATTC CCGAGGGCGA CGACCCCTCT CTCAAGACTC CTAAAGTCT CGGACTGGC GTGACAGACA CGGCCACCGA  
 225 A R C C K G P L P T D C C H E Q C A A G C T G P K H S D C L A C L H  
 235  
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 295  
 301 GCCTGCCACC CCTGTCTCTCC GATGTGTAAG GGCTCCCGCT GCTGGGGGAGA GAGTTCTGAG GATTGTGAGA GCCTGACGCG CACTGTCTGT GCCGGTGGCT  
 311 CGGACGGTGG GGACAAGAGG CTACACATTC CCGAGGGCGA CGACCCCTCT CTCAAGACTC CTAAAGTCT CGGACTGGC GTGACAGACA CGGCCACCGA  
 325 A C H P C S P M C K G S R C W G E S S E D C Q S L T R T V C A G G C  
 335  
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 395  
 401 GTGCCCCGCTG CAAGGGGCCA CTGCCCCACTG ACTGCTGCCA TGAGCAGTGT GCTGCCGGCT GCACGGGCC CAAGCACTCT GACTGCCCTGG CCTGCCTCCA  
 411 CACGGGCGAC GTTCCCGGT GACGGGTGAC TGACGACGGT ACTCGTCACA CGACGGGCCA CGTCCCGG GTTCGTGAGA CTGACGGACC GGACGGAGGT  
 425 A R C C K G P L P T D C C H E Q C A A G C T G P K H S D C L A C L H  
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FIG. 7H



[illegible]

425



# VARIABLE HEAVY DOMAIN

	10	20	30	40
2C4	EVQLQQSGPELVKPGTSVKISKAS	[GFTFTDYTMD]	WVKQS	*
	** ** *	* ** *		*
574	EVQLVESGGGLVQPGGSLRLS	CAAS [GFTFTDYTMD]	WVRQA	
		** * *		
hum III	EVQLVESGGGLVQPGGSLRLS	CAAS [GFTFSSYAMS]	WVRQA	
	50	a	60	70
2C4	HGKSLEWIG [DVNPN	SGGSIYNQRFKG]	KASLTVD	RSSRIVYM
	* *	**	*** *	**** *
574	PGKLEWVA [DVNPN	SGGSIYNQRFKG]	RFTLSVD	RSKNTLYL
	*****	*** ****	* * *	
hum III	PGKLEWVA [VISGD	GGSTYYADSVKG]	RFTISRDN	SKNTLYL
	abc	90	100ab	110
2C4	ELRSLTFEDTAVYYCAR	[NLGPSFYFDY]	WGQGT	TLTVSS
	*** **		**	
574	QMNSLRAEDTAVYYCAR	[NLGPSFYFDY]	WGQGT	TLTVSS
		*****		
hum III	QMNSLRAEDTAVYYCAR	[GRVGYSLYDY]	WGQGT	TLTVSS

FIG. 1

# Variable Light Domain

	10	20	30	40
2C4	DTVMTQSHKIMSTSVGDRVSITC	[KASQDVSIGVA]	WYQQRP	*
	**	**** *		
574	DIQMTQSPSSLASVGDVRTITC	[KASQDVSIGVA]	WYQQKP	*
		* ** ***		
hum KI	DIQMTQSPSSLASVGDVRTITC	[KASQDVSIGVA]	WYQQKP	
	50	60	70	80
2C4	GQSPKLLIY [SASYRYT]	GVPDFRTGSGSGTDFTTISSVQA		*
	**	* *		*
574	GKAPKLLIY [SASYRYT]	GVPSRFSGSGSGTDFTLTISSLQP		*
		* ****		
hum KI	GKAPKLLIY [AASSLES]	GVPSRFSGSGSGTDFTLTISSLQP		
	90	100		
2C4	EDLAVYYC [QQYVIYPYT]	FGGGTKLEIKRT		*
	*	*		
574	EDFATYYC [QQYVIYPYT]	FGQGTKVEIKRT		*
		*** *		
hum KI	EDFATYYC [QQYNSLPWT]	FGQGTKVEIKRT		

FIG. 2

# Maytansinoids (DM1)

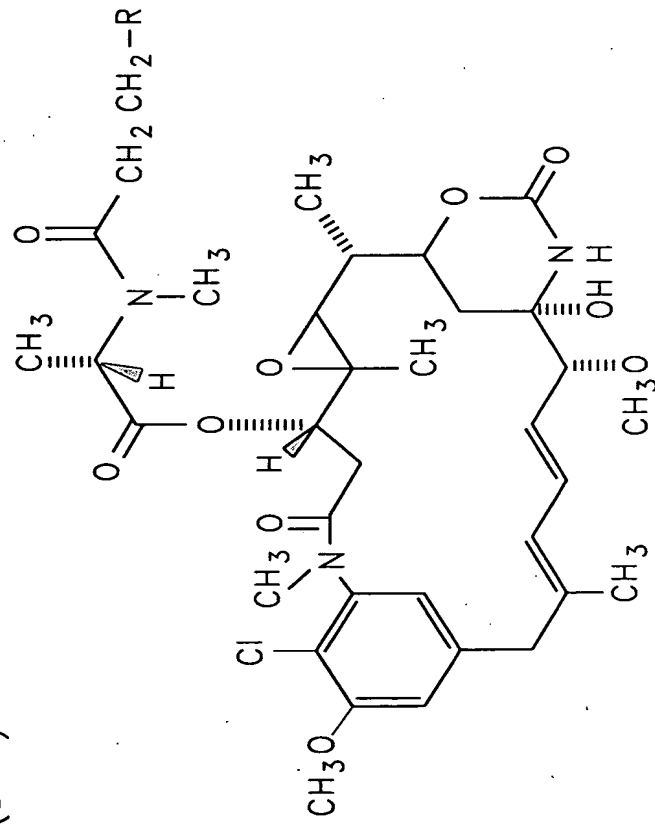
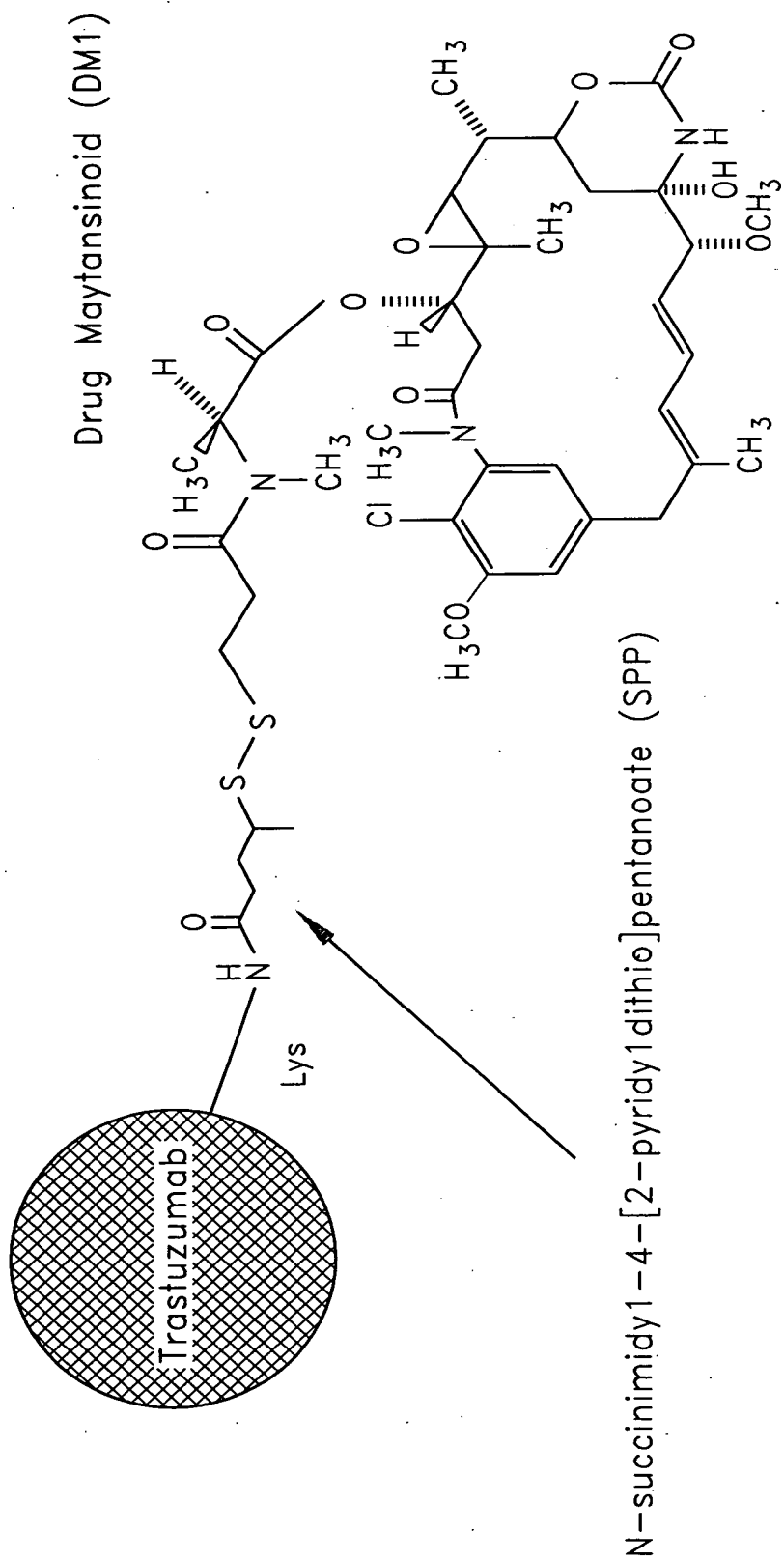


FIG. 3



**FIG. 4**

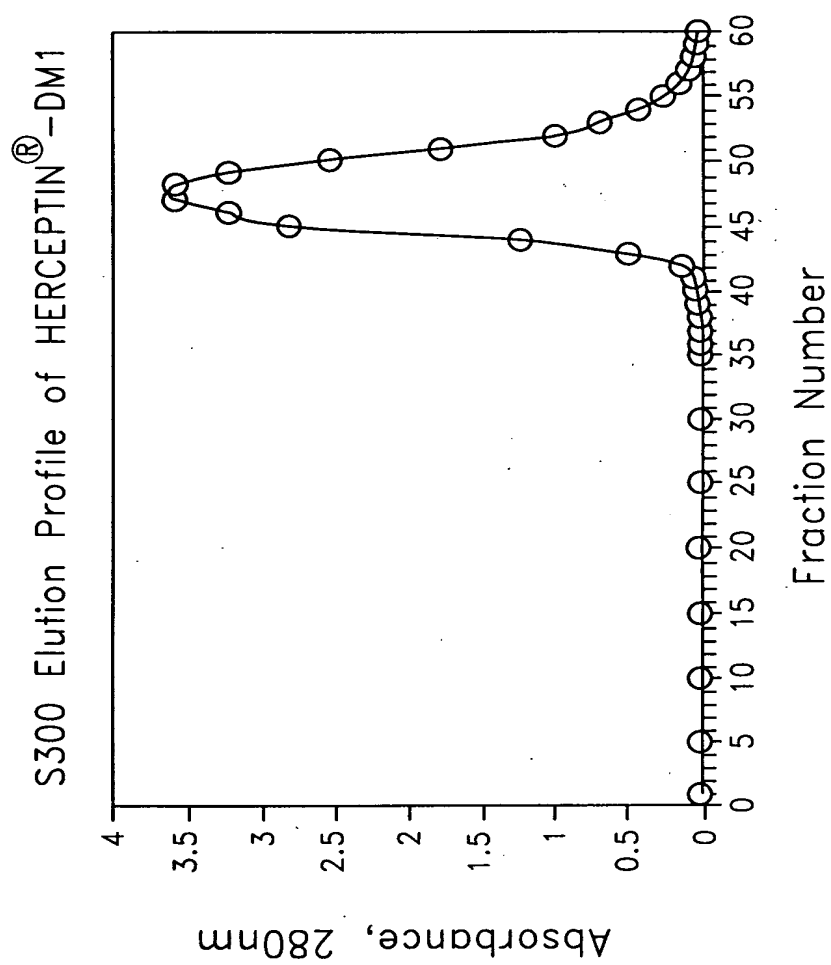


FIG. 5

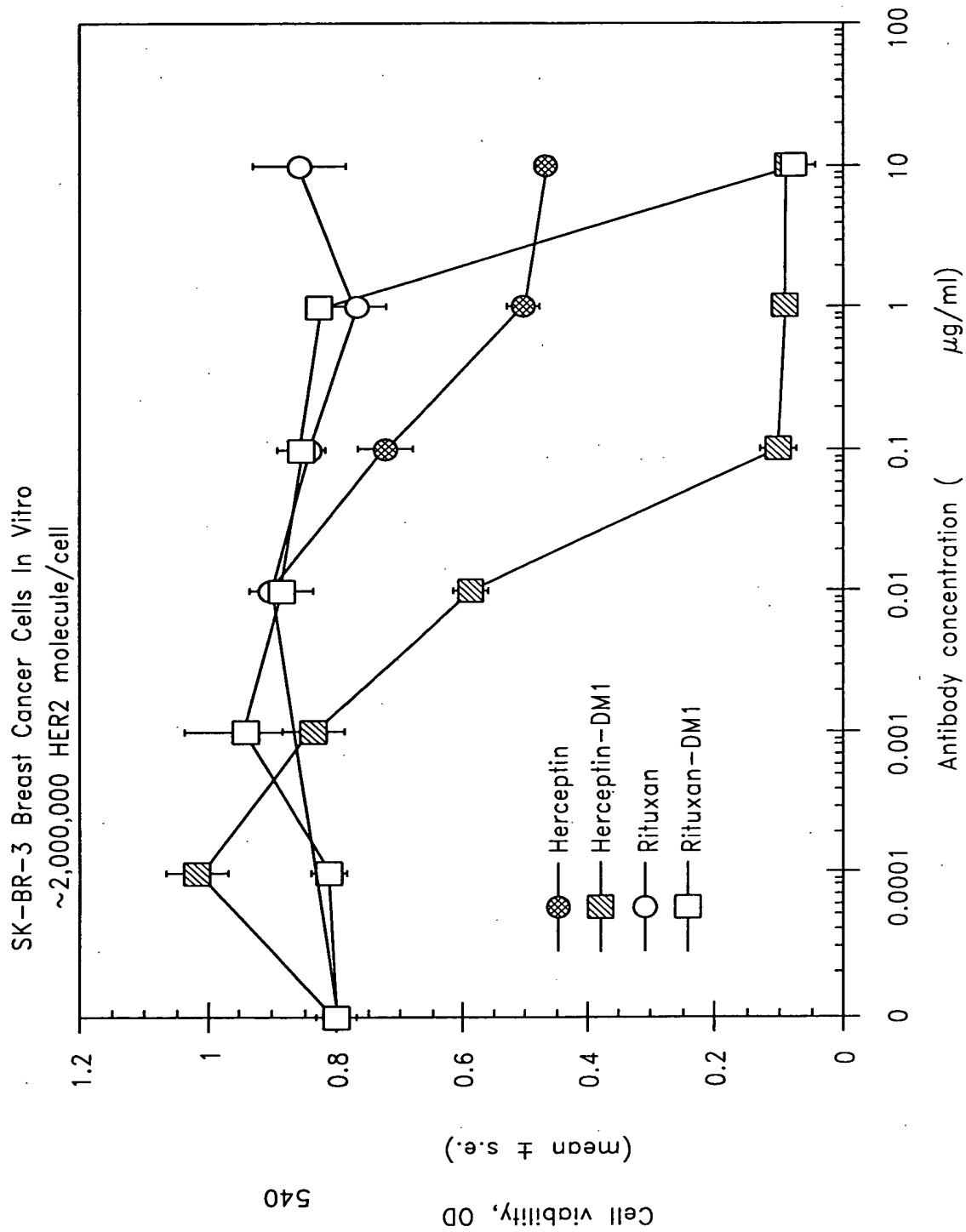


FIG. 6